

# **FIGURE 1**

GGACTAATCTGTGGGAGCAGTTATTCCAGTATCACCCAGGGTGAGCCACACCAGGACTGT  
GTTGAAGGGTGTTCCTTAAATGTAATACCTCCTCATCTTCTTACACAGTG  
TCTGAGAACATTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTTTAGGAGGA  
CTACTCTCTCTGACAGTCCTAGACTGGTCTTACACTAAGACACCATGAAGGAGTATGTG  
CTCCTATTATTCCCTGGCTTGCTCTGCCAACCCCTTACACATCGCACT  
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATG  
ATGATGATGAGGACAACCTCTTTCCAACAAGAGAGCCAAGAACCCATTTC  
TTTGATCTGTTCCAATGTGTCATTGGATGTCAGTGTCTTACGAGTTGTACATTGCTC  
AGATTAGGTTGACCTCAGTCCAAACCAACATTCCATTGATACTCGAATGCTTGTACATTGCTC  
AAAACAATAAAATTAAAGGAAATCAAAGAAAATGATTAAAGGACTCACTTCACTTATGGT  
CTGATCCTGAACAACAAGCTAACGAAGATTACCCAAAAGCCTTCTAACCAACAAAGAA  
GTTGCGAAGGCTGTATCTGCCCACAACTAACTAAGTGAACATCCACTTAATCTTCCAAAT  
CATTAGCAGAACTCAGAATTCAATGAAAATAAGTTAAGAAAATACAAAGGACACATTCAA  
GGAATGAATGCTTACACGTTGGAAATGAGTGCAAACCCCTTGTGATAATAATGGGATAGA  
GCCAGGGGCATTGAAAGGGTGACGGTGTCCATATCAGAATTGCGAACAGAAAATGACCT  
CAGTCCTAAAGGCTTACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTCA  
ACAGTGGAACTTGAGGATTTAAACGATAAAAGAAACTACAAAGGCTGGGCTAGGAAACAA  
CAAATCACAGATATCGAAAATGGGAGTCTGCTAACATACCAACGTGTGAGAGAAATACATT  
TGGAAAACAATAAAACTAAAAAAATCCCTCAGGATTACCAAGAGTTGAAATACCTCCAGATA  
ATCTCCTTCATTCTAATTCAATTGCAAGAGTGGAGTAAATGACTTCTGTCCAACAGTGCC  
AAAGATGAAGAAATCTTATACAGTCAATAAGTTATTCAACAACCCGGTAAATACTGGG  
AAATGCAACCTGCAACATTCTGTTGTTGAGCAGAATGAGTGTCACTGGAACTTT  
GGAATGTAATAATTAGTAATTGTAATGTCCATTAAATATAAGATTCAAAATCCCTACATT  
TGGAAACTTGAACCTTAAATGGTAGTTATATACAGCAAAATATCTATTCTCA  
AGTGGTAAGTCCACTGACTTATTGACAAGAAATTCAACGGAATTGGCCAAACTATT  
GATACATAAGGGTTGAGAGAAACAAGCATCTATTGAGCTTCTTGTGCTACAAATGAT  
CTTACATAAAATCTCATGCTTGACCATTCTTCTTCATAACAAAAAGTAAGATATTGGTA  
TTAACACTTGTATCAAGCACATTAAAGAACTGTACTGTAAATGGAATGCTTGACT  
TAGCAAAATTGTGCTTCTTCTTGTGTTAGAAAAACAGAATTAAACAAAGACAGTAATGT  
GAAGAGTGCATTACACTATTCTTATTCTTAGTAACCTGGTAGTACTGTAATATTAAAT  
CATCTTAAAGTATGATTGATATAATCTTATTGAAATTACCTTATCATGCTTAGAGCCGT  
CTTATGTTAAAACATAATTCTTAAAGCCTTCAGTAAATGTTATTACCAACTTGA  
TAAATGCTACTCATAAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTAATTATT  
ACCTGATTAAAAATCTCTGTTAAACGTGTAGTGTTCATAAAATCTGTAACCTCGCATT  
AATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC  
TTCAACTCTAAGGAATATTTGAGATATCCCTTGGAAAGACCTGCTTGGAAAGAGCCTGGA  
CACTAACAAATTCTACACCAAAATTGCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA  
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAACCGAAAGCTCTA  
TATAATGCTCAGAGTTCTTATGTATTCTTATTGGCATTCAACATATGAAAATCAGAAA  
ACAGGGAAATTTCATTAAAAATTGGTTGAAAT

## **FIGURE 2**

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392
<subunit 1 of 1, 379 aa, 1 stop
<MW: 43302, pI: 7.30, NX(S/T): 1
MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKLRRLYLSHNQLSEIPLNLPKSLAELRIHENVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPEL
KYLQIIFLHSNSIARGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM
```

**Signal sequence.**

amino acids 1-15

**N-glycosylation site.**

amino acids 281-285

**N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

**Leucine zipper pattern.**

amino acids 154-176

## **FIGURE 3**

CGGACGCGTGGCGGACCGTGGGCCCGCAGCAGCCCCGGCCCTCCGCCCTCCGACTCGGCCCTCC  
CTCCCTCCGCCGCTCCCGCCCTCCCTCCCTCCCTCCCTCCCCAGCTGCTCCGCTCGCAGCTGCCGAGCCTCC  
GGCCCCGCCGCCCGCTGCTGCTCCTCGGGCTGCTGCTGCTCGCCTCCCCGCCGGCCGGCCGGCCAGA  
GCCCGCCCGTGTGCCCCATCCGTTCTGAGAAGGAGCCGCTGCCCCTCGGGGAGCGGAGGGCTGCACCTTCGGCG  
GAAGGTCTATGCCCTGGACGAGACGTGGCACCCGGACCTAGGGCAGGCATTGAGGTGATGCGCTGCGTGTG  
CGCCGAGGCCCTCAGTGGGTGCGCGTACCAAGGGCCCTGGCAGGGTCAAGCTGCAAGAACATCAAACAGA  
GTGCCCAACCCGGCCTGGGCAGCCGCGCAGCTGCCGGACACTGCTGCCAGACCTGCCAGGGCAG  
CAGTTGCGAGGCCAGCCGAGCGGCCCTGCTCGAGTATCGCGGGACCCGGAGCATCGAGTTAGCGACCG  
CGGGGAGCCAGGCCTGAGGAGCGGGCCCTGGTGACGCCACACGGACTTCGCTGGCGTGTGACAGGGCGAG  
GTCGCAAGCGGTGGCACGAGCCCAGTCTCGTGTGCGCTCTAGCCTCCGCTCTATCTCCTACAGGGCGCT  
GGACGCCCTACCAGGATCCGTTCTCAGACTCCAATGGCAGTGTCTGTTGAGCACCCCTGCAGCCCCCACCA  
AGATGGCCTGGTCTGTTGGGTGAGGCCAGTGCCTCGGTTGCTCTGCGGCTCCTTAGGGCAGAACAGCTGCA  
TGTGGCACTTGTGACACTCACTCACCCCTCAGGGGAGGTCTGGGGCCTCTCATCGGCACCGGGCCTGGCTGC  
AGAGACCTTCAGTGCCATCCTGACTCTAGAAGGCCCCCACAGCAGGGCGTAGGGGCATCACCTGCTCACTCT  
CAGTGACACAGAGGACTCCCTGCTATTGCTGCTCTTCGAGGGCTGCTGGAAACCAGGAGTGGGGACTAAC  
CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGCAGCTACTGCGAGAACCTCAGGCCATGTCAGCCCA  
GGAACCAGGCTTGCTGAGGTGCTGCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGTGGGGAGCTGCA  
GATGGCCCTGGAGTGGCAGGCAGGGCAGGGCTGCGCATAGGACACATTGCTGCCAGGAAGAGCTGCGACGT  
CCTGCAAAGTGCCTTGTGGGCTGATGCCCTGATCCCAGTCCAGACGGGTGCTGCCGCTCAGCCAGCCTCAC  
GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGGCCATGACACT  
GGAGACCAAGCCTCAGCGGAGGGATCAGCGCACTGTCCTGTGCCACATGGCTGACTCCAGGCCAGGAGGACACAC  
GGCGTGGGTATCTGCCCTGGCTGGGTGCCAGGGCTCATATGCTGCTGAGAATGAGCTCTCTGAACGT  
GGGACCAAGGACTCCAGACGGAGAGCTCGGGGACGTGGCTGCCCTACTGTGGCATAGCGCCCG  
CCATGACACGCTGCCGTGCCCTAGCAGGAGCCCTGGTGTACCCCTGTGAAGAGCCAAGCAGCAGGGCACGC  
CTGGCTTCTGGATACCCACTGTCACCTGCACTATGAAGTGTGCTGGCTGGCTTGGTGTGAACAAG  
CACTGCACTGCCACCTCTGGGCCCTCTGGAACGCCAGGGCCTGGCGGCTGCTGAAGGGATTCTATGGCTC  
AGAGGCCAGGGTAGCCCCAGAGGGAGCTCGAGGGCAGGTGACATAGCCAACCATGTGAGGTGGCG  
GATCACCACCAAGGGTAGCCCCAGAGGGAGCTCGAGGGCAGGTGACATAGCCAACCATGTGAGGTGGCG  
ACTGCGCTGGAGGCCGGGGCCAGGGGTGCGGGGCTGGGGCTCCGATACAGCCTCTGCTGCCGCC  
TGTGGTGCCTGGTCTCCGGCCCTAGGCCGCCAAACCTGGTGGTCTGGGGCCCGAGACCCCAACACATG  
CTTCTCGAGGGCAGCGCCCCACGGGCTCGCTGGGCCAACTACGACCCGCTGCTCACTGCA  
CTGCCAGAGACGAACGGTGATCTGACCCGGTGTGCCACCGCCAGCTGCCACACCCGGTGAGGCTCC  
CGACCAGTGCCTGCCCTGTTGCCCTGAGAAACAGATGTCAGAGACTTGCAGGGCTGCCAGGAAGAGCCGGACCC  
AGGAGAGGGCTGCTATTGATGGTGAACGGAGCTGGCGGGCAGCGGGTACGGGTGACTGTGAGAAGGTGAGTG  
CTTGGCTTAATTAAGTGTGCTGTCACCTGCAAGGGGGCACTGGAGAGGTGACTGTGAGAAGGTGAGTG  
TCCCCGGCTGCCCTGTGCCACGCCCTGCGTGTCAACCCACCGACTGCTGCAAACAGTGTCCAGTGGGTGG  
GGCCCACCCAGCTGGGGACCCCATGCAAGGGCTGATGGGCCGGCTGCCCTTGTGGCAGTGGTCCC  
AGAGAGTCAGAGCTGGCACCCCTCAGTGGCCCTTTGGAGAGATGAGCTGTATCACCTGAGATGTGGGGCAGG  
GGTGCCTACTGTGAGGGGATGACTGTTACTGCCACTGTCCTGTGGCTGGGAGAGGAGTCAGTGTG  
CCGCGTGCACGGCCACCGCGGCCAGAGACCAACTGATCCAGAGCTGGAGAAAGAACCGAAGGCTCTA  
GGGAGCAGCCAGAGGGCCAAGTGAACAGAGGATGGGCTGAGCTGGGAAGGGGTGGCATCGAGGACCTTCTT  
GCATTCTCTGTGGGAAGCCCAGTGCCTTGTCTCTGCTGCCCTACTCCCACCCCAACTACCTCTGGGAA  
CCACAGCTCCACAAGGGGGAGAGGCCAGCTGGGCCAGACCGAGGTCAAGCCACTCCAAGTCTGCCACCC  
TCGGCCTCTGTCTGGAGCCCCACCCCTTCTCTGACATAATGTCAGTGGCTGTTGGATTTTAATT  
TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG  
TTTGTATTATAACATTCTTTCAAGTCAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 4**

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pi: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLGLLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE  
TWHPDLGQPFGVMRVCVLCACEAPQWGRRTGRGPRVSKNIKPECPTPACGQPRQLPGHCCQT  
CPQERSSSERQPSGLSFEYPRDPEHRSYSRDRGEPEGAERARAGDGHDFVALLTGPRSQAVER  
ARVSLLRSSLRFSISYRRLLRPTRIRFSDSNGSVLFEHPPAAPTQDGLVCGVWRAPRSLRL  
LRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSDTED  
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLREIQANVSAQEPGFAEVLPNLTVQEMD  
WLVLGELQMALEWAGRPGRLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN  
GSLIYQVQVVGTSSEVVAMTLETKPQRRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML  
LQNELFLNVGKTDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS  
LDTHCHLHYEVLLAGLGGSEQGTVAHLLGPPGTPGPRLLKGFYGSEAQGVVKDLEPELLR  
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGLREAAGAEGVRALGAPDTASAAPPV  
PGLPALAPAKPGGPGRPRDPNTCCFFEGQQRPHGARWAPNYDPLCSLCTCQRRRTVICDPVVCP  
PPSCPHVQAPDQCCPVCPEKQDVRLPGLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPPF  
GLIKCAVCTCKGGTGEVCEKVCQCPRLACAQPVRVNPTDCKQCPVGSGAHPQLGDPMQADG  
PRGCRFAGQWFPEQSWHPSVPPFGEMSCITCRCGAGVPHCERDDCSLPLSCGSGKESRCCS  
RCTAHRRPPETRTDPELEKEAEGS

**Signal sequence.**

amino acids 1-23

**N-glycosylation sites.**

amino acids 217-221, 351-355, 365-369, 434-438

**Tyrosine kinase phosphorylation sites.**

amino acids 145-153, 778-786

**N-myristoylation sites.**

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,  
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,  
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,  
905-911

**Amidation site.**

amino acids 87-91

**Cell attachment sequence.**

amino acids 165-168

**Leucine zipper pattern.**

amino acids 315-337

## FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCGTCACTGCG  
TCCTGGCTCCGGCTCCCGGCCCTCCCGGCCATGAGCCCCGCCGCGCCAGGCGCCCGGTGCGCAGCTGC  
TGCCCGCGCTGGCCCTGCTGCTGCTGCTGGAGCGGGGCCCGAGGAGCAGCTCCCTGCCAACCCGGTGCCCC  
CCCGGCCCTGTCTGCCGCCGGCGTGCAGCCCTGCCGAATGGGGTGTGCACTCGCAGCTCCGGATCTCCGG  
AGCCGGACCCCGCAGCACCCGCCCGCCGGAGCCTGGCTACAGCTGCACCTGCCCGCCGGATCTCCGG  
CCAAGTGCAGCTTGTGCAGATCCTGTGCAGCAACCCGGTGTACCGATGGCAACTGCAGCAGCAGCAGCA  
GCAGCAGCGATGGCTACCTCTGCATTGCAATGAAGGCTATGAAGGTCCAAGTGTGAACAGGCACTTCCAGTC  
TCCAGCCACTGGCTGGACCGAATCCATGGCACCCGACAGCTTCAGCCTGTTCTGCTACTCAGGAGCCTGACA  
AAATCCTGCCTCGCTCTCAGGCAACGGTGAACACTGCCTACCTGGCAGCCAAAACAGGGCAGAAAGTTGTAGAAA  
TGAAATGGGATCAAGTGGAGGTGATCCCAGATATTGCTGTGGGAATGCCAGTCTAACAGCTCTGGGGTGGCC  
GCCTGGTATCCTTGAAAGTGCACAGAACACCTCAGTCAAGATTGCCAGATGCCACTGCCACTGATTG  
TCTGGAAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGCAGAAGTGTGACCCCCCTCAGGCTT  
CAGGGGACTGGCTCTGGAGGAGATGCTGCCCTGGGAATAATCACTTATTGGTTTGTGAATGATTCTG  
TGACTAAGTCTATTGGCTTGCGCTTAACCTGGTGGTGAAGGTCAAGCACCTGTGTGCCGGGGAGAGTCAG  
CAAATGACTGGAGTGTTCAGGAAAAGGAAAATGCACACAGAACGCCAGAGGCAACTTTCTGTACCTGTG  
AGGAGCAGTACGTGGGTACTTCTGTGAAGAACAGTGCATGCTTGCCAGAGGAAACCTTGCCAAAACAACCGCAGCT  
GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTCACCTGTGTTGCCCTCTGGTTACTGGAGAGCTT  
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTCCAGTCTCAGTGGAT  
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTAAGAAAAGGTGACCCCTGCGCCTCGTCTCCGT  
GCCAGAACACGGCACCTGCTATGGACGGGTACACTTACCTGCAACTGCAGCCGGGCTTCACAGGGCGA  
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCAGCGTGGGACCAGCT  
ACAAATGCCCTGTGATCAGGTTACCATGGCCTCTACTGTGAGGAGGAATAATGAGTGCCTCTCGCTCCAT  
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGCTGGCAGAACATCAAAGGAACAC  
ACTGTGAATTGTACAAGGATCCCTGCGTAACGTCAGCTGCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA  
ATGGCACGTGCATCTGTGCACCCGGTTACAGGTGAAGAGTGCACATTGACATAATGAATGTGACAGTAACC  
CCTGCCACCATGGGGAGCTGCCCTGGACCAGCCAAATGGTTATAACTGCCACTGCCCATGGTGGTGGAG  
CAAACGTGAGATCCACCTCAATGGAAGTCCGGGACATGGCGAGAGCCTCACCAACATGCCACGGACTCCC  
TCTACATCATCATTGGAGCCCTCTGCGTGGCTTCATCCTTATGCTGATCATCCTGATGTGGGATTGCGCA  
TCAGCCGCATTGAATACCAGGGTTCTCCAGGGCAGCCTATGAGGAGTTCTACAACTGCCAGCATGACAGCG  
AGTCAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTGGAAAGAAATCCGGCTGCAATGTATGATGTGA  
GCCCATGCCATTGAAGATTACAGTCTGATGACAACACCTGGTCACACTGATTAAAACAAAGATTGTAAT  
CTTTTTGGATTATTTCAAAAGATGAGATACTACACTCATTTAAATATTTAAGAAAATAAGCTTAA  
GAAATTAAAATGCTAGCTGCTCAAGAGTTTCAGTAGAATATTAAGAACTAATTTCTGCAGCTTGTGTT  
GAAAAAAATATTTAAAACAAAATTGTGAAACCTATAGACGATGTTAATGTACCTTCAGCTCTAAACTGT  
GTGCTTCTACTAGTGTGCTCTTCACTGTAGACACTATCACGAGACCCAGATTAATTCTGTGGTTTACA  
GAATAAGTCTAATCAAGGAGAAGTTCTGTTGACGTTGAGTGCCGCTTCTGAGTAGAGTTAGAAAACCAC  
GTAACGTAGCATATGATGTATAATAGAGTATAACCGTTACTAAAAAGAAGTCTGAAATGTTGTTGGAAA  
AGAAACTAGTTAAATTACTATTCTAACCGAATGAAATTAGCCTTGCCTTATTCTGTGCAAGGTAAGTAAC  
TTATTCTGCACTGTTGTTGAACTTGTGAAACATTCTTCAGGTTGTTGTCATTTCGTAACAGTCG  
TCGAACTAGGCTCAAAACATACGTAACGAAAGGCCAGCGAGGAAATTCTGATTGATTGAACTATATT  
TTCTTAAAGTCAAGGGTTCTATATTGTGAGTAAATTAAATTACATTGAGTTGTTGCTAAGAGGTAG  
TAAATGTAAGAGAGTACTGGTCTTCAGTAGTGAGTATTCTCATAGTGCAGCTTATTATCTCCAGGATGTT  
TTTGTGGCTGTATTTGATTGATATGTGCTTCTGATTCTGCTAATTCCAACCATATTGAATAATGTGATC  
AAGTCA

## **FIGURE 6**

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQQLPALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR  
PEPDHQHPAPAGEPGYSCTCPAGISGANCQLVADPCASNPCHGNCSSSSSSDGYLCICM  
EGYEGPNCEQALPSLPATGWTESMAPRQLQPVATQEFDKILPRSQATVTLPTWQPKTGQKV  
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ  
QCSLIDGRSVTPLQASGLVLEEMLALGNNFIFGVNDSVTKSIVALRLTLVVKVSTCVPG  
ESHANDLECSGKGKCTKPSEATFSCTCEEQYVGTCEEYDACQRKPCQNNASCIDANEKQD  
GSNFTCVCLPGYTGELCQSKIDYCILDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC  
ASSPCQNNGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCSRSGTSYKCLCDPG  
YHGLYCEEYNECLSAPlNAATCRDLVNGYECVCLAELYKGTHCELYKDPCANVSLNGATC  
DSDGLNGTCICAPGFTGEEDIDINECDSNPCHGGSCLDQPNNGYNCHCPHGWVGANCEIHL  
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILELIIVGICRISRIEYQGSSRPAYEEFYN  
CRSIDSEFSNAIASIRHARFGKKSRPAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

**Signal sequence.**

amino acids 1-28

**Transmembrane domain.**

amino acids 641-660

**N-glycosylation sites.**

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568

**Glycosaminoglycan attachment site.**

amino acids 320-324

**Tyrosine kinase phosphorylation sites.**

amino acids 490-498, 674-682

**N-myristoylation sites.**

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571

**Amidation site.**

amino acids 702-706

**Aspartic acid and asparagine hydroxylation site.**

amino acids 520-532, 596-608

**EGF-like domain cysteine pattern signatures.**

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

## **FIGURE 7**

CTCTGGAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTCAGGCTTCAGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA  
ATCACTTATTGGTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC  
CTGGTGGTGAAGGTCA~~GC~~ACCTGTGTGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC  
AGGAAAAGGAAAATGCACCACGAAGCCGT~~CA~~GAGGCAACTTTCTGTACCTGTGAGGAGC  
AGTACGTGGGTACTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTGCCAAACAAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATT~~C~~ACCTGTGTTGCCTTCC  
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGAG

## **FIGURE 8**

CTCTGGAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTCAGGCTTCAGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAAATA  
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCCTTAAC  
CTGGTGGTGAAGGTCA~~GCAC~~CTGTGCCGGGGAGAGTCACGCAAATGACTTGGAGTGTTC  
AGGAAAAGGAAAATGCACCGAAGCCGT~~CA~~GAGGCAACTTTCTGTACCTGTGAGGAGC  
AGTACGTGGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAACAAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATT~~C~~ACCTGTGTTGCCTTCC  
TGGTTATACTGGAGAGCTTGCCAACCGA~~ACT~~GAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGAG

## **FIGURE 9**

GCTGAGTCTGCTGCTCCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG  
GCCCCCCCAGAGCCCTCACCAACGCTGGCGCCCCAGAGCCCACACCATGCCGGCACCTAC  
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGCCCT  
GATGCGGGACTTCCCGCTCGTGGACGCCACAACGACCTGCCCTGGTCCTAAGGCAGGTTT  
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGGCCAGACCAGCCTGGAC  
AGGCTTAGAGATGGCCTCGTGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA  
GGACCGGGATGCCCTGCGCCTCACCCCTGGAGCAGATTGACCTCATGCCGATGTGCCT  
CCTATTCTGAGCTGGAGCTGTGACCTCGCTAAAGCTCTGAACGACACTCAGAAATTGGCC  
TGCCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT  
CTACATGCTGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGCAGAGA  
GCTCCGCTAAGGGGTCCACTCCTCTACAACAAACATCAGCGGGCTGACTGACTTTGGTGAG  
AAGGTGGTGGCAGAAATGAACCGCCTGGCATGATGGTAGACTTATCCCATGTCTCAGATGC  
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTCTCCACTCGCTGCC  
GGGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAAGCTCTGAAGAAGAAC  
GGTGGCGTCGTGATGGTGTCTTGTCCATGGAGTAATACAGTCAACCCATCAGCCAATGT  
GTCCACTGTGGCAGATCACTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGA  
TTGGTGGAGATTATGATGGGCCGCAAATTCCCTCAGGGGCTGGAAGACGTGTCCACATAC  
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCC  
TCGTGGAAACCTGCTCGGGCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC  
AAAGCCCCTGGAGGACAAGTTCCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTC  
TCACGTCTCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACACTCACTGAGATTCCCATA  
CTGGACAGCCAAGTTACCAAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG  
TCCTTGCAGTTGTGGCACCTTCCCAGTCCTTATTCTGTGGCTCTTGATGACCCAGTTAGTCC  
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA  
AATATTCTGAAATAATGTTGGACATAG

## **FIGURE 10**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595
<subunit 1 of 1, 433 aa, 1 stop
<MW: 47787, pI: 6.11, NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCA SYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIIELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQS PLEDKFPDEQLSSS
CHSDLRRLQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLA VVATFPVLLWL
```

**N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

**N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

**Renal dipeptidase active site.**

amino acids 134-157

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## **FIGURE 11**

AAAACCTATAATATTCCGGATTATTCAACCGTCCCACCATGGGCGGGATCCGGCGGCCG  
CGAATTCTAAACCAACATGCCGGCACCTACGCTCCCTGACCAACACTCAGTAGTCCCAGCA  
CCCAGGGCCTGCAAGAGCAGGCACGGGCCTGATGCGGGACTTCCGCTCGTGGACGGCCAC  
AACGACCTGCCCTGGTCCTAACGGCAGGTTACCAGAAAGGGCTACAGGATGTTAACCTGCG  
CAATTCAGCTACGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCCAGT  
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG  
CAGATTGACCTACGCCGATGTGCGCTCCTATTCTGAGCTGGAGCTTGTGACCTCGC  
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTAGAGGGTGGCCACTCGC  
TGGACAATAGCCTCTCCATCTTACGTACCTTACATGCTGGAGTGCCTACCTGACGCTC  
ACCCACACCTGCAACACACCCGGCAGAGAGCTCCGCTAACGGCGTCCACTCCTTACAA  
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGCAGAAATGAACCGCCTGGCA  
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG  
GCACCTGTGATCTTCTCCCACCGCCTGGCGGGTGTGTGCAACAGTGCTCGGAATGTTCC  
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTGCCATGG  
GAGTAATAACAGTGCAACCCATCAGCCAATGTGTCCTGTGGCAGATCACTCGACCACATC  
AAGGCTGTCTGGATCCAAGTTACCGGATTGGAGATTATGATGGGCCGGCAAATT  
CCCTCAGGGCTGGAAGACGTGTCACATACCGGCTGTGATAGAGGAGTTGCTGAGTCGTG  
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCGTGGAACCTGCTGCCTGGCTTCAGACAA  
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTGGAGGACAAGTCCGGATGA  
GCAGCTGAGCAGTCCCTGCCACTCCGACCTCTCACGTCTCGTCAGAGACAGAGTCTGACTT  
CAGGCCAGGAACACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA  
GTCTCAGAGTCCTCCCCCACCCTGACAAAACACATGCCACCGTGCCTGGCAGCACCTGA  
ACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCAAAACCCAAGGACACC

## **FIGURE 12**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX (S/T) : 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCAZYSELELVTSAKALND
TQKLACLIGVEGGSLDNSLSILRTFYMLGVRYLTLTHCNTPWAESSAKGVHSFYNNISGL
TDFGEKVAEMNRLGMMVDSLHVSADAARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDDYDGAGKFPQGLE
DVSTYPVLIIELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDKTHTCPPCPAPELLGGP
SVFLFPPKPKDT
```

## **FIGURE 13**

CGCCCAGCGACGTGCGGGCGGCCTGGCCCGGCCCTCCCGCGCCCGGCCTGCGTCCCGGCC  
CTGCGCCACCGCCGCCGAGCCGCAGCCCGCCGCCGGCAGCGCCGGCCCCATGCCC  
GCCGGCCGCCGGGGCCCCGCCGCCAATCCGCGGGCGGCCGCCGTTGCTGCCCTGCT  
GCTGCTGCTCTGCGTCTCGGGCGCCCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA  
GTCCCCAGGATCCCACGCTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA  
GACCCACCAGGAGCCACCGCCGAGGGCCTACTGGACCCCTAACGGCGCCGCTGCC  
TGAGCTCTCCCGTGTACTCAACGCCCTCACCTGGCTCTGGCCCTGGCCAACCTCAATGGGT  
CCAGGCAGCGGTGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATTGGCTGGC  
TCCTGCCTCTATGTTGGCTGCCCTAGAGAAACCGTCAACATCAGCTGCTGGTCCAAGAA  
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGAGACCTCCTCACACCA  
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGCCAGGACAACACATGTGAGGAGTAC  
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGAT  
CTGGGTGGAGGCCACCAACGCCCTGGCTCTGCCGCTCCGATGTACTCACGCTGGATATCC  
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGACGTGAGCCCGTGGGGCCTGGAG  
GACCAGCTGAGCGTGCCTGGGTGTCGCCACCCGCCCTCAAGGATTCTCTTCAAGCAA  
ATACCAAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGAGCATTGAGCA  
ACCAGACCTCCTGCCGCTGCCGGCTGAAACCCGGCACCGTGTACTCGTCAAGTGC  
TGCAACCCCTTGGCATCTATGGCTCCAAGAAAGCCGGATCTGGAGTGAGTGGAGGCC  
CACAGCCGCTCCACTCCCCCAGTGAGCGCCGGCCGGCGCGGGCGTGCAGACCGC  
GGGGCGGAGAGCCGAGCTGGGGCGGTGCGCGAGCTCAAGCAGTTCTGGCTGGCTC  
AAGAACCGCGTACTGCTCCAACCTCAGCTCCGCTCTACGACCAAGTGGAGCCTGGAT  
GCAGAACGTGCAACAAGACCCGAACCAAGGACGAGGGATCCTGCCCTGGGAGACGGGCA  
CGGCGAGAGGTCTGCCAGATAAGCTGTAGGGCTCAGGCCACCTCCCTGCCACGTGGAGA  
CGCAGAGGCCGAACCAAACGGGGCACCTCTGAGCTCCAACGCCATAACAGCTCTGACT  
CCTCAGCAGGAGCTGGGTGGCCCTGAGCTCCAACGCCATAACAGCTCTGACT  
GAGGCCACCTTGGGTGACCCAGTGGGTGTGTGTGTGAGGGTTGGTTGAGTTGC  
CTAGAACCCCTGCCAGGGCTGGGGTGAGAAGGGAGTCATTACTCCCCATTACCTAGGGC  
CCTCCAAAAGAGTCCTTTAAATAATGAGCTATTAGGTGCTGTGATTGTGAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAACAAAAAAA

## FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV  
HGDPPGATAEGLYWTLNGRRLLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL  
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTGAHGETFLHTNYSLKYLWYGQDNTCEE  
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGG  
LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSDWKVVDDVSNQTSCRLAGLKPGTVYFVQ  
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGACEPRGGEPPSGPVRRELKQFLG  
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

**Signal sequence.**

amino acids 1-30

**Transmembrane domain.**

amino acids 44-61

**N-glycosylation sites.**

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 413-417

**N-myristoylation sites.**

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,  
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

**Amidation site.**

amino acids 3-7, 79-83, 411-415

**Growth factor and cytokines receptors family signature 2.**

amino acids 325-331

## **FIGURE 15**

CCCCACCGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAACACACCAACGCTCGCAGCCACAAAAGGGATGAAATTCTTCTGGACATCCTC  
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCCCTAA  
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGGTGCCAAGGTTACACCTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGCACATTCTGGACTACAAA  
GGCATTCTTCTGCAATGACGAAGAATAACCATTGCCATTGTCACTGTGGCTTCGGCAG  
CTGGACATGTCTCGGTCCCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGTTGGA  
TTTCATAAAACTTGACAGATGAACGGCTGCCTACAAATAACTGGAGTCACAAACACATG  
TCTGTCCTAATTCGAAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCC  
CTCTGGAACCTGAGGAAGTGGAACAGGCTGATGCATGGATTCTGACTGAGCAGAACAGATG  
ATTTTTATTCCATCTCTATAGCTTTAAACAACATTGAAAGGATCCTCCTGAGCGTT  
CCTGGCAGTTAAAAGAAAAACTAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATAGCACCTAGTTCTGAAAACGTGTTAAGTTGATGCAGTTATTGGATATAAAATGA  
ATAGTGCCAGAATTAAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA  
TCATTTTGAGGCTTGGCAGTCTCATTACTACCACCTGTTCTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTTGCTCACCTGAAGGCTTGCAA  
AATTGTACCATAACGTTATTAAACATATATTATTATTGATTGACTTAAATTGTTG  
ATAATTGTGTTCTTTCTGTTCTACATAAAACTGAAACCTCAAGCTCTAAATAAAA  
TGAAGGACTATATCTAGGGTATTCAACATGAAATCATGAACTCTCAATGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCCAATGCCAACATTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGATTAAAG  
GAGAATTGAGAGAAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAA  
AA  
AA

## FIGURE 16

```
</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436
<subunit 1 of 1, 300 aa, 1 stop
<MW: 32964, pI: 9.52, NX(S/T): 1
MKFLLDILLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ
```

**Signal sequence.**

amino acids 1-19

**Transmembrane domain.**

amino acids 170-187

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 30-34, 283-287

**N-myristoylation sites.**

amino acids 43-49, 72-78, 122-128, 210-216

## **FIGURE 17**

GAATGTTCTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAAGGACTG  
GGGTGACGGCAGGGCAGGGCGCCTGGCGGGAGAAGCGCGGGCTGGAGCACCACAA  
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGAGCCGGAGGGGGACT  
GCGAGAGGACCCGGCGTCCGGCTCCGGCTCCGGCTCCAGGCACGCCGGCACCATGGCAGCCAGGGCTTGCCGGCCG  
TGCTCCTGGCCTGGCGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC  
CCGGGGCACCCGGCCTCCAGGCACGCCGGCACCATGGCAGCCAGGGCTTGCCGGCCG  
CGATGGCCGCGACGGCCGCGACGGCGCCGGCTCCGGAGAGAAAGGCAGGGCGGG  
GGCCGGGACTGCCGGGACCTCGAGGGACCCGGCGAGGAGAGGCAGGGACCCGGGG  
CCCACCGGGCTGCCGGGAGTGCTCGCTCCGCATCCGCCTTCAGCGCCAAGCGCTC  
CGAGAGCCGGGTGCCTCCGCGTCTGACGCACCCCTGCCCTCGACCGCGTGTGGTGAACG  
AGCAGGGACATTACGACGCCGTACCGCAAGTTCACCTGCCAGGTGCCTGGGTCTACTAC  
TTCGCCGTCCATGCCACCGTCTACCGGCCAGCCTGCAGTTGATCTGGTGAAGAATGGCGA  
ATCCATTGCCTCTTCTTCCAGTTTCGGGGGTGGCCAAGCCAGCCTCGCTCTCGGGGG  
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC  
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTCTCCGGATTTCTGGTGTACTCCGA  
CTGGCACAGCTCCCCAGTCTTGCTTAGTGCTGCAGCAGTCATCCAGGAGGGCTGGCCCCCTGGAAATATT  
TAGAAGGAGGGTGTGAGGCTGACAACCAAGGTCATCCAGGAGGGCTGGCCCCCTGGAAATATT  
GTGAATGACTAGGGAGGTGGGTAGAGCACTCTCCGTCTGCTGGCAAGGAATGGGAAC  
AGTGGCTGTGCGATCAGGTCTGGCAGCAGGGCAGTGGCTGGATTCTGCCAACGACCA  
GAGGAGTGTGCTGTGCTGGCAAGTGTAAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT  
GGGGTGCTCTTCTGGTCCCTGCTTCTGGATCCTCCCCACCCCTCCTGCTCCTGGG  
GCCGGCCCTTTCTCAGAGATCACTCAATAAACCTAAGAACCTCATAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLLLLGLAAGSPPPLDDNKIPSLCPGHPGLPGTPGHGSQGLPGRDGRDGRDGAPGAP  
GEKGEGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP  
FDRV LVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP  
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

**Signal sequence.**

amino acids 1-15

**N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

**Cell attachment sequence.**

amino acids 77-80

## **FIGURE 19**

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG  
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT  
GCTGCATCCAGAGACCTCCCCTGGCCGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTG  
GCACCACCTGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC  
CTGAACAGGAAGGAGAGTTCTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGTCCA  
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAAGTGGCTCAAG  
CCAGGGCAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCTGTGGCGCACCTG  
CAAGTGGGCTGGAACATGCAGCTGCTGCCGCGGCTTGGCTCCTTGTGAAGTGGTCAG  
CCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCCAGGAGAGTGTGCTCGCAACGCCA  
CCTGCACCCACTACACGCAGCTCGTGTGGCCACCTCAAGCCAGCTGGCTGTGGCGGCAC  
CTGTGCTCTGCAGGCCAGACAGCGATAGAACGCTTGTCTGTGCCTACTCCCCGGAGGCAA  
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGGCTCTGCA  
CAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGACCATGCAGGGGGCTCTGTGAGGTCCCC  
AGGAATCCTGTGCGATGAGCTGCCAGAACCATGGACGTCTAACATCAGCACCTGCCACTG  
CCACTGTCCCCCTGGCTACACGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC  
ACGGCCGGTCCGGAGGAGGAGTGCTCGTGTGACATCGGCTACGGGGAGGCCAG  
TGTGCCACCAAGGTGCATTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT  
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG  
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGCCGC  
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATGGCT  
CACCTACAAGACGCCAAGGACTCCTCCGCTGGCCACAGGGAGCACCAGGCCTCACCA  
GTTTGCTTTGGCAGCCTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGTTT  
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCCTCAACTGGAACGACCAGCGCTGCAAAC  
CCGAAACCGTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGCCAGGGCCT  
GAGCCTGACCACATGGCTCCCTGCCCTGCCCTGGAGCACGGCTCTGCTTACCTGTCTGC  
CCACCTGTCTGGAACAAGGGCAGGTTAAGACCACATGCCCTATGTCAAAGAGGTCTCAGA  
CCTTGCACAATGCCAGAAGTGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCAGGGAGTG  
AGTGTAGAAGAAGCTGGGCCCTCGCCTGCTTGTGATTGGAAAGATGGCTCAATTAGA  
TGGCGAAGGAGAGGACACGCCAGTGGTCAAAAAGGCTGCTCTTCCACCTGGCCAGAC  
CCTGTGGGCAGCGGAGCTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAG  
CTGAAAAA

0  
1  
2  
3  
4  
5  
6  
7  
8  
9

## **FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176  
<subunit 1 of 1, 455 aa, 1 stop  
<MW: 50478, pI: 8.44, NX(S/T): 2  
MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLSLHNRLRSWV  
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV  
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCAGQTAIEAFVCAYSPGG  
NWEVNGKTIIPYKKGAWSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCH  
CHCPPGYTGRYQVRCQLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC  
FMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLTTNEVTDSDFETRNFWIG  
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK  
TRNRYICQFAQEHISRWGP  
**Signal sequence.**  
amino acids 1-26  
**Transmembrane domain.**  
amino acids 110-124  
**N-glycosylation sites.**  
amino acids 144-148, 243-247  
**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 45-49  
**N-myristoylation sites.**  
amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,  
288-294, 331-337, 398-404  
**Prokaryotic membrane lipoprotein lipid attachment site.**  
amino acids 204-215  
**EGF-like domain cysteine pattern signature.**  
amino acids 249-261, 280-292  
**C-type lectin domain signature.**  
amino acids 417-442

## **FIGURE 21**

CGGACGCGTGGCTGGCGCTGCAAAGCGTGTCCGCCGGTCCCCGAGCGTCCCAGCCCT  
CGCCCCGCC**ATG**CTCTGCTGCTGGGCTGTGCCTGGGGCTGTCCCTGTGTGGGTGCGA  
GGAAGAGGCCAGAGCTGGGCCACTCTCGGAGCAGGATGGACTCAGGGTCCCAGGGCAAG  
TCAGACTGTTGCAGAGGCTGAAAACAAACCTTGTGACAGAATTCTCAGTGAAGTCTACC  
ATCATTTCCCGTTATGCCTTCACTACGTTCTGCAGAATGCTGAACAGAGCTTCTGAAGA  
CCAGGACATTGAGTCCAGATGCAGATTCCAGCTGCAGCTTCATCACCAACTCACTATGC  
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGTAGG  
GTAAAAGAGAAAAGGAATAAAACCACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTAG  
AGCTTCTGCAGTGAATTCCCAGCAAGGACAAAGCCCTTTCTGAGTTATGAGGAGCTTC  
TGCAGAGGCCCTGGCAAGTACGAGCACAGCATCAGCGTGGGCCAGCAGCTGCC  
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATGCATCCCTGGAGGTGCTGCC  
GCTTCACAACAGCAGGCAGAGGGGAGTGGCGGGGAAGATGATTCTGGGCCTCCCCAT  
CTACTGTCAATTAAACAAAATGAAACATTTGCCAACATAATTAAACCTACTGTAGTACAA  
CAAGCCAGGATTGCCAGAATGGAATTGGAGACTTATCATTAGATATGACGTCATAG  
AGAACAGAGCATTGGGACATCCAGGTTCTAAATGGCTATTTGTGCACTACTTGTCTCTA  
AAGACCTTCCTCTTACCCAAAGAATGTGGTATTGCTGCTTGACAGCAGTGTCTTATGGT  
GGAACCAAACCCGGCAGACCAAGGATGCCCTCTCACAAATTCTCCATGACCTCCGACCCCA  
GGACCGTTCACTATTGGATTTCCAACCGATCAAAGTATGGAAGGACCACTGATAT  
CAGTCACTCAGACAGCATCAGGGATGGAAAGTGTACATTACCATATGTCACCCACTGGA  
GGCACAGACATCAACGGGCCCTGCAGAGGGCATCAGGCTCTCAACAAGTACGTGGCCCA  
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTCCTGACGGATGGGAAGGCCACGG  
TCGGGAGACGCACACCCCTCAAGATCCTCAACAAACACCCGAGAGGCCGCCAGGCCAGTC  
TGCATCTTCACCATTGGCATCGCAACGACGTGGACTTCAGGCTGCTGGAGAAACTGTCGCT  
GGAGAACTGTGGCTCACACGGCGGTGACAGGAGGAGGACGCAGGCTCGCAGCTCATCG  
GGTCTACGATGAAATCAGGACCCCGCTCTCTGACATCCGATCGATTATCCCCCAGC  
TCAGTGGTGCAGGCCACCAAGACCCCTGTTCCCAACTACTTCAACGGCTGGAGATCATCAT  
TGCAGGGAAAGCTGGTGACAGGAAGCTGGATCACCTGCACGTGGAGGTACCGCCAGCAACA  
GTAAGAAATTCATCATCCTGAAGACAGATGTGCTGTGCGGCCCTCAGAAGGCAGGGAAAGAT  
GTCACAGGAAGCCCCAGGCCTGGAGGGCGATGGAGAGGGGACACCAACCACATCGAGCGTCT  
CTGGAGCTACCTCACCAAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGAACGATGAACCGG  
AGAAGGAGCGGCTGGCAGGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCACTCCC  
TTCACCTCCATGAAGCTGAGGGGCCGGTCCACGCATGGATGGCCTGGAGGAGGCCACGG  
CATGTCGGCTGCCATGGGACCCGAACCGGTGGTCAGAGCGTGCAGGAGCTGGCACGCAGC  
CAGGACCTTGCTCAAGAAGCCAAACTCCGTAAAAAAAAACAAAACAAAACAAAAAAAAGA  
CATGGGAGAGATGGTGTGTTCTCCACCACTGGGATACGAT**TGAGAAGATGCCACCT**  
GCAAGCCAGGAAGACGCCCTCACCAAGACACCATGTCTGCTGGCACCTGATCTGGACCTC  
CCAGCCTCCAGAACTGTGAGAAATAATGTGTTAAGCTAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA

## FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192  
<subunit 1 of 1, 694 aa, 1 stop  
<MW: 77400, pI: 9.54, NX(S/T): 6  
MLLLLGLCLGLSLCVGSQEEAQSWGHSSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIIS  
RYAFTTVSCRMLNRASEDQDIEFQMQIPAAAFITNFTMLIGDKVYQGEITEREKSGDRVKE  
KRNKTTEENGEKGTEIFRASAVIPSVDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS  
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR  
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFVLDSSASMVGTK  
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVIHHMSPTGGTD  
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNNTREAARGQVCIF  
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV  
QATKTLFPNYFNGSEIIIAAGKLVDRKLDHLHVEVTASNNSKKFIILKTDVPVRPQKAGKDVTG  
SPRPGGDGEGLTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS  
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKQNKTKKRHGR  
DGVFPLHHLGIR

**Signal sequence.**

amino acids 1-14

**N-glycosylation sites.**

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

**Glycosaminoglycan attachment sites.**

amino acids 213-217, 391-395

**N-myristoylation sites.**

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

## **FIGURE 23**

CGGACGCGTGGGTGCCCGAC**ATG**GCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC  
GGCAGCGGGCGGCGGCCCTCCCGGGCTCCGGCTTGCTGTTGCTCTCTCCGCCGCGG  
CACTGATCCCCACAGGTGATGGCAGAACTGTTACGAAAGACGTGACAGTGATCGAGGGA  
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCACTGAA  
TCCCAACAGGCAGACCATTATTCAGGGACTTCAGGCCTTGAAGGACAGCAGGTTTCAGT  
TGCTGAATTTCAGTGAACCTAAAGTATCATTGACAAACGTCTCAATTCTGATGAA  
GGAAGATACTTTGCCAGCTCTACCGATCCCCACAGGAAAGTTACACCACATCACAGT  
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG  
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTCAA  
GGGAACACAGAGCTAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC  
CAGTCAGCTGATGCTGAAGGTGACAAGGAGGACATGGGTCCAGTGAATCTGCCAGGTGG  
AGCACCCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT  
CAAGTGCACATTCAAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA  
GTTAACATGTGAAGCCATCGGAAGCCCCAGCCTGTGATGGTAACCTGGTGAGAGTCGATG  
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCAACCTGTTCATCAATAACCTAAACAAA  
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGAAAGCTCACTCGGATTA  
TATGCTGTATGTATACGATCCCCCACAACATCCCTCCTCCCACAACAACCACCA  
CCACCACCACCACCAACCATCCTTACCATCATCACAGATTCCGAGCAGGTGAAGAAGGC  
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTGGCGGTGGTGGTGGTGGTGGTGG  
GCTGTGCTTGCATCATTCTGGGCGCTATTGCAAGACATAAGGTACATACTTCACTC  
ATGAAGCCAAGGAGGCCATGACGCAGCAGACAGCAGCTATAATCAATGCAGAAGGA  
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATC**TAG**ATCAGCCTTTGTTCAAT  
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

## **FIGURE 24**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTTELKG
KSEVEEWSDMYTVTSQMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDEMPQHAVLSPNLFINNLNKTDNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVFAMLCLLIIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI
```

**Signal sequence.**

amino acids 1-36

**Transmembrane domain.**

amino acids 372-393

**N-glycosylation sites.**

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,  
430-434

**Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

**N-myristoylation sites.**

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432

## FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGA  
CCGCCAGGAAAGACTGAGGCCGCGCCTGCCCGCCGGCTCCCTGCGCCGCGCCGCTC  
CCGGGACAGAAGATGTGCTCCAGGGCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT  
GGGGCCTGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCACAGACAGTCTTCT  
GCACTGCCGCCAGGGACCACGGTCCCCGAGACGTGCCACCCGACACGGTGGGCTGTAC  
GTCTTGAGAACGGCATCACCATGCTGACGCAAGCAGCTTGCCGGCTGCCGGCCTGCA  
GCTCCTGGACCTGTACAGAACAGATGCCAGCCTGCCCTGCCCTGCCGCTGCTGCTGG  
ACCTCAGCCACAACAGCCTGCCCTGGAGGCCGATCCTGGACACTGCCAACGTGGAG  
GCGCTGCCGTGGCTGGTCTGGGCTGCAGCAGCTGGACGAGGGCTCTCAGCCGTTGCG  
AACCTCCACGACCTGGATGTGTCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG  
GCCTCCGGGCCTGACGCCCTGCCCTGGAGGCCAACACCCGCAATTGCCAGCTGCCGCC  
GAGGACCTGCCGGCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAACGCTGCCAGGC  
CCTGCCTGGCAGCCTCTGCCCTCTTCCCCCCTGCCCTGCGCTGCTGGCAGCTGCCCAACC  
CCTTCAACTGCGTGTGCCCTGAGCTGGTTGGCCCTGGTGCAGGAGAGGCCACGTCACA  
CTGCCAGCCCTGAGGAGACGCCGCTGCCACTTCCCACCAAGAACGCTGCCGGCTGCTCCT  
GGAGCTTACTACGCCGACTTGGCTGCCAGCCACCACACCAGCCACAGTGCCACCA  
CGAGGCCCGTGGTGCAGGAGGCCACAGCCTGTCTTAGCTTGCTCCTACCTGGCTTAGC  
CCCACAGGCCGCCACTGAGGCCAGGCCACTGCCCACTGCCAACCGACTGTAGGGCC  
TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCCAATGGGGCACATGCCACCTGG  
GGACACGGCACCACCTGGCGTCTGTGCCCTGAAGGCTTCAGGGCCTGTACTGTGAGAGC  
CAGATGGGGCAGGGACACGCCAGGCCACACCAGTCAGGCCAGGCCACCACGGTCCCT  
GACCCCTGGCATCGAGCCGGTGAGCCCCACCTCCCTGCCGTGGGCTGCAGCGTACCTCC  
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATGCAACCTATGGGCCCTGAT  
AAGCGGCTGGTACGCTGCGACTGCCCTCGCTCGCTGAGTACACGGTACCCAGCTGCG  
GCCCAACGCCACTTACTCCGTCTGTGTCATGCCCTTGGGGCCGGGCGGGTGCCGGAGGGCG  
AGGAGGCCTGCCGGAGGCCACACCCCCAGCCGTCACCTCAACCACGCCAGTCACC  
CAGGCCCGAGGGCACCTGCCCTCATTGCCCGCCCTGGCGCGGTGCTCCTGGC  
CGCGCTGGCTGCCGTGGGGCAGCCTACTGTGTGCCGGGGGGCCATGGCAGCAGCGG  
CTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCACTTGGAACTGGAGGGAGTGAAGGTC  
CCCTTGAGGCCAGGCCAGGCCAACAGAACAGGGCAGCTGGGGCCTCTCAGCCAGTGAGATGGC  
GTGTGAGGTGCCACTCATGGCTTCCAGGGCCTGGCCTCCAGTCACCCCTCACGCAAAGC  
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCGGCTCTCAGCCAGTGAGATGGC  
CAGCCCCCTCTGCTGCCACACCACGTAAGTCTCAGTCCCAACCTGGGATGTGTCAGA  
CAGGGCTGTGACACAGCTGGGCCCTGTTCCCTCTGGACCTGGTCTCCTCATGTGAG  
ATGCTGTGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCTATGAGGACAGTGT  
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC  
GCATGCCCTGGGCCCTGCTGGCTCTCCACTCCAGGCCAGGACCTGGGGCCAGTGAAGGAAG  
CTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGACTCTAGTCTTGGCCCCAGG  
AAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTAGAACATGTTTGTCTTTAA  
AATATATATATATTATAAGAGATCCTTCCCATTATTCTGGGAAGATGTTTCAAAC  
AGAGACAAGGACTTGGTTTGTAAAGACAAACGATGATATGAAGGCCTTGTAAAGAAAAA  
ATAAAAAAAAAAA

## **FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804  
<subunit 1 of 1, 598 aa, 1 stop  
<MW: 63030, pI: 7.24, NX(S/T): 3  
  
MCSRVPLLLPLLLLALGPGVQGCPSCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN  
GITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGIILDTANVEALRL  
AGLGLQQLDEGLFSRLRNLHLDLVSDNQLERVPPVIRGLRGLTRRLLAGNTRIAQLRPEDLA  
GLAALQELDVSNLSQLALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWRESHVTLASP  
EETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAP  
ATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQ  
GTRPSPTPVTPRPPRSLTGLIEPVSPSLRVGLQRYLQGSSVQLRSLRTYRNLSGPDKRLV  
TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE  
GNLPLLIAPALAAVLLAALAAVGAAAYCVRRGRAMAAAQDKGQVGPAGPLELEGVKVPLEP  
GPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI  
  
**Signal sequence.**  
amino acids 1-23  
  
**Transmembrane domain.**  
amino acids 501-522  
  
**N-glycosylation sites.**  
amino acids 198-202, 425-429, 453-457  
  
**Tyrosine kinase phosphorylation site.**  
amino acids 262-270  
  
**N-myristoylation sites.**  
amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571  
  
**Prokaryotic membrane lipoprotein lipid attachment site.**  
amino acids 14-25  
  
**EGF-like domain cysteine pattern signature.**  
amino acids 355-367  
  
**Leucine zipper pattern.**  
amino acids 122-144, 194-216

## **FIGURE 27**

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCCTACCCGCCACC  
TCCTTGCTACCCCACTCTTGAACACAGCTGTTGGCAGGGTCCCCAGCTC**ATGCCAGCCTC**  
ATCTCCTTCTTGCTAGCCCCAAAGGGCCTCCAGGAAACATGGGGGCCAGTCAGAGAGC  
CGGCACTCTCAGTTGCCCTTGTTGAGTTGGGGCAGCTCTGGGGCCGTGGCTGTGCC  
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA  
GGGGACAGGAGGCCCTCCCAGAATGGGAAGGGTATCCCTGGCAGAGTCCTCCGGAGCAGA  
GTTCCGATGCCCTGGAAGCCTGGAGAATGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC  
ACCCAAAAACAGAAGAAGCAGCACTCTGCTGCACCTGGTCCCATTACGCCACCTCAA  
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGAGAGGCCTAC  
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTATCTGCTGTATAGCCAGGTC  
CTGTTCAAGACGTGACTTCACCATGGTCAGGTGGTCTCGAGAAGGCCAAGGAAGGCA  
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCCGGACCGGGCTACAACAGCT  
GCTATAGCGCAGGTGTCTTCATTACACCAAGGGATATTCTGAGTGTCTACATTCCCCGG  
GCAAGGGCGAAACTAACCTCTCCACATGGAACCTCCTGGGTTGTGAAACTG**TGATT**  
GTGTTATAAAAGGGCTCCAGCTTGGAAAGACCAAGGGTGGTACATACTGGAGACAGCAA  
GAGCTGAGTATATAAGGAGAGGAATGTGCAGGAACAGAGGCATCTCCTGGGTTGGCTC  
CCCGTTCCCTCACTTTCCCTTTCATTCCCACCCCTAGACTTGATTACGGATATCTG  
CTTCTGTTCCCCATGGAGCTCCG

## **FIGURE 28**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27433, pI: 9.85, NX(S/T): 2
MPASSPFLLAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQLSRREV
SRLQGTGGPSQNGEYPWQSLPEQSSDALEAWENGERSRKRAVLTQKQKKQHSVLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFMGQVVSREG
QGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSHGTFLGFVKL
```

**Signal sequence.**

amino acids 1-40

**N-glycosylation site.**

amino acids 124-128

**Tyrosine kinase phosphorylation site.**

amino acids 156-164

**N-myristoylation site.**

amino acids 36-42, 40-46, 179-185, 242-248

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 34-45

## FIGURE 29

CACTTCTCCCTCTTCTTACTTCGAGAAACCGCGCTCCGCTCTGGTCGCAGAGAC  
CTCGAGACCGCGCCGGGAGACGGAGGTGCTGGTGGGGGGACCTGTGGCTGCTCGTA  
CCGCCCCCCCACCCCTCTTCTGCACTGCCGTCTCCGAAGACCTTTCCCTGCTCTGTT  
TCCTCACCGAGTCTGTGCATGCCCGGACCTGGCGGGAGGAGGCTGGCCGGCGGGAGA  
TGCTCTAGGGCGGCGGGAGGAGCGGCCGGACGGAGGGCCGGCAGGAAGATGGC  
TCCCGTGGACAGGGACTCTTGTGGCGTACTGCCGTCTTGCTCTGGCCTCTGGCCTGGT  
CCTGAGTCGTGTGCCCATGTCCAGGGGAACACGAGGAGTGGAGGGACTGAGGAGCTGC  
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACACATGAAAAATACAGGCCAGTCAG  
GACCAGGGCTCCGTCTCCGGCTGCTGCCGTGCTGTGACCCCGTACCTCATGTACCC  
GGCGACCGCCGTGCCCATGCAACATCACTATCTGAAAGGGAGAAGGGTGAACGGAG  
ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGCCAGGGCCACACTGGA  
CCCAAAGGGCAGAAGGGCTCCATGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCC  
CTTTTGTGGGCCGGAAGAACGCCATGCAACAGCAACCACTACTACAGACGGTGATCTCG  
ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTCACCGCAAGTTCTACTGCTAC  
GTGCCCGGCCTCTACTTCTCACGCCCAACGTGACACCTGAAACCAGAAGGAGACCTACCT  
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTGCGCAGGTGGCGACCGCAGCA  
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACAGGTGTGGTACGCCTC  
TACAAGGGCAACGTGAGAACGCCATCTCAGCGAGGAGCTGGACACCTACATCACCTCAG  
TGGCTACCTGGTCAAGCACGCCACCGAGCCTAGCTGGCCGGCACCTCTTCTCGCC  
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTCCCGATCCCTGGACTCCGACTC  
CCTGGCTTGGCATTCAAGTGAGACGCCCTGCACACAGAAAGCCAAGCGATCGGTGCTCC  
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGGGCACCGC  
GAGAACCTCTGGGACCTCCCGGCCCTCTGCACACATCCTCAAGTGAACCCGCACGGC  
GAGACGGGGTGGCGCAGGGCGTCCAGGGTGGCAGCGCGGTCCAGTCCTGGAAATA  
ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG  
TTGTTATTTGTCTTCCAGCCAGCCTGCTGGCTCCAAAGAGAGAGGGCTTTCAGTTGAG  
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGTGAGGGAGGGCCGGGGCAGG  
AAACTACCTCTGGCTTAATTCTTAAAGCCACGTAGGAACCTTCTTGAGGGATAGGTGGACC  
CTGACATCCCTGTGGCCTTGCCAAGGGCTCTGCTGGTCTTGAGTCACAGCTGCGAGGT  
GATGGGGCTGGGCCAGGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCGCTGGCTTGGC  
TCCAGGTTGGTAGAAGCAGCGAAGGGCTCTGACAGTGGCCAGGGACCCCTGGTCCCCA  
GGCCTGAGATTTCTATGAGGGCAGAGCTCCTGGTACATCCATGTGAGCTGCTCC  
ACCCCTGTGCCACCCAGAGCCCTGGGGGTGGTCTCCATGCCCTGGCATCGGCT  
TTCTGTGCCCTCCCACACAAATCAGCCCCAGAAGGCCGGGCTTGGCTTGTGTTTT  
TATAAAACACCTCAAGCAGCACTGCACTCCATCTCCTCGTGGCTAACATCACCCT  
CCACGTGTGTTGGCTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCTACTGCCCT  
CATCCAGGCCTCTGACCACTAGCCTGAGAGGGCTTTCTAGGCTTCAAGCAGCAGGGAGAG  
CTGGAAGGGCTAGAAAGCTCCGCTGTGTTCTCAGGCTCCTGTGAGCCTCAGTCAGGAG  
AGACCAGAGTCAGAGGAAGTACACGTCCAAATCACCGTGTCAAGGATTCACTCTCAGGAGC  
TGGGTGGCAGGAGAGGAATAGCCCCGTGGCAATTGCAGGACAGCTGGAGCAGGGTTGCG  
GTGTCTCCACGGTGCCTCGCCCTGCCATGCCACCCAGACTCTGATCTCCAGGAACCC  
ATAGCCCCCTCCACCTCACCCATGTTGATGCCAGGGTCACTCTGCTACCCGCTGGGCC  
CCCAAACCCCGCTGCCCTCTTCCCTCCCCCATCCCCCACCTGGTTTGACTAATCCTGC  
TTCCCTCTCTGGCCTGGCTGCCGGATCTGGGTCCCTAACGTCCTCTCTTAAAGAAACTT  
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGCGTGGCCGAAGCAGAGCGCACACTC  
GCTGCTTAAGCTCCCCAGCTTCCAGAAACATTAAACTCAGAATTGTGTTTCAA

## **FIGURE 30**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQLLLAYCLLLAFASGLVLSRVPVHQVGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVLFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP
```

**Signal sequence.**

amino acids 1-25

**N-glycosylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

**Amidation site.**

amino acids 150-154

**Cell attachment sequence.**

amino acids 104-107

## **FIGURE 31**

GC GGAGCATCCGCTCGGGTCTCGCCGAGACCCCCGCGCGGATTGCCGGTCTCCCGCG  
GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGCGCCGGGTCTCGACGCCA  
GAGAGAAATCTCATCATCTGTGCAGCCTCTTAAAGCAAACTAAGACCAAGGGAGGATTAT  
CCTTGACCTTGAAGACCAAAACTAAACTGAAATTAAAT**TGTTCTCGGGGGAGAAGGGAG**  
CTTGACTTACACTTGGTAATAATTGCTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
GCCTCAAAAAGAGTCTAGAAGATGTTGCATTGACATCCAGTCATCTCTAAGGGAATC  
AGAGGCAATGAGCCCGTATAACTTCAACTCAAGAAGACTGCATTAATTCTGCTGTTCAAC  
AAAAAACATATCAGGGACAAAGCATGTAACCTGATGATCTCGACACTCGAAAAACAGCTA  
GACAACCCAACTGCTACCTATTTCTGCTCCAAACGAGGAAGCCTGTCCATTGAAACCAGCA  
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCCATCTTGACCAGAAATTGCAAG  
CCAAGAGTTACCCCAGGAAGATTCTCTTACATGCCAATTTACAAGCAGTCACTCCCC  
TAGCCCACATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTCT  
CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTAAAGATGGATGAAGCAAGTGCCA  
GCTCCTGCTTATAAGGAAAAGGCCATTCTCAGAGTTACAATTTCTCTGATCAAGAAA  
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCCAGCTACGGTGGCAGTTGCTCTCCA  
CATACCACCTCGGCTACTCCAAAGCCGCCACCCCTCTACCCACCAATGCTCAGTGCACACC  
TTCTGGACTTCCCAGCCACAGCTGGCACCACAGCTCCACCTGTAACCACTGTCACTTCTC  
AGCCTCCCACGACCCCTCATTTACAGTTTACACGGCTCGGGCTACACTCCAAGCAATG  
GCTACAACAGCAGTTCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTAGA  
AACCATACCGTTACAGAAATCTCAAACTTAACCTTGAACACAGGGATGTGTATAACCCTA  
CTGCACTTCTATGTCAAATGTGGAGTCTTCACTATGAATAAAACTGCTCCTGGAGGTT  
AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTCCAGAAAATCAGTACGGCCTTCC  
ATTGAAAAATGGCTTCTTATGGGTCCCTGCTCTTGTTGTCCTGGTGTAGGCC  
TCGTCTCTGGTAGAATCTTCACTCCGCAGGAAACGTTACTCAAGACTGGAT  
TATTGATCAATGGATCTATGTGGACATC**TAA**GGATGGAACCTGGTGTCTCTTAATTCTT  
TAGTAACCAGAAGCCAAATGCAATGAGTTCTGCTGACTGCTAGTCTTAGCAGGAGGTTG  
TATTGAGACAGGAAATGCCCTCTGCTTCTTGTGAGACAGGGTT  
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTGGCTCTCACCGAACCTCGTCTC  
CTGGGTTCAAGCGATTCTCTGCCTCAGCCTCTAAGTATCTGGATTACAGGCATGTGCCA  
CCACACCTGGGTGATTTGTATTTAGTAGAGACAGGGTT  
GTCTCAAACCTGACCTAGTGATCCACCCCTCTGGCCTCCAAAGTGTGGATTACAGG  
CATGAGCCACCACAGCTGGCCCTCTGTTATGTTGGTTTGAGAAGGAATGAAGTG  
GGAACCAAATTAGGTAAATTGGTAATCTGCTCTAAATATTAGCTAAAACAAAGCTCT  
ATGTAAGTAATAAGTATAATTGCCATATAAAATTCAAACATTCAACTGGCTTTATGCAA  
GAAACAGGTTAGGACATCTAGGTTCCAATTCACTCACATTCTGGTTCCAGATAAAATCAAC  
TGTGTTATCAATTCTAATGGATTGCTTTCTTTTATATGGATTCTTAAACTTATT  
CCAGATGTAGTTCTCCAATTAAATTTGAATAATCTTGTACTCAA

## **FIGURE 32**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGLTYTLVII CFLTLRLSASQNLKKSLEDVVIDIQSSLKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMI FDTRKTARQPN CYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTT LISTVFTRAATLQAMATTAVLTTFQAP
TDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI
```

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321

## **FIGURE 33**

GCGGCACCTGGAAG**TG**CGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGGTGGTCTTC  
GCCTCCTTGTGTGCCTGGTATTGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT  
GTCCAGTGCTGCCTATAGCATCCGCAGCATGGGGAGAGGCCTGCCTCAAAGCTCCAGTCC  
CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA  
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAATCTGCTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACGGGA  
ATGTGACAGCAACACGATGTTGATATGTATGAAGGCATAACTCTGGACCGATGACAAAG  
TTTATTCAAGGTGCTGCCAAATCCCTGCTCTCATGGTGACCTATGACGACGGAAGCAC  
AAGACTGAATAACGATGCCAAGAATGCCATAGAACGACTTGGAAAGTAAAGAAATCAGGAACA  
TGAAATTCAAGGTCTAGCTGGGTATTATTGCAGCAAAAGGCTTGGAACTCCCTCCGAAATT  
CAGAGAGAAAAGATCAACCACCTGATGCTAAGAACACAGATATTCTGGCTGGCCTGCAGA  
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAG**TG**ACACTGCAGGGCCTGAGTAAAT  
GTGTTCTGTATAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTCTAAATCCAACA  
GCCCATATTGATGAGTATTGGTTGTTGAAACCAATGAACATTGCTAGTTGTATCA  
AATCTTGGTACGCAGTATTATTACCAAGTATTGATGAGATGTCAATTAGCAGGA  
AACTAAAATGAATGGAAATTCTTAAAAAAAAAA

0 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

## **FIGURE 34**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
><subunit 1 of 1, 235 aa, 1 stop
><MW: 25982, pI: 9.09, NX(S/T): 2
MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMDYEGDNGSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAAEIQIEGCIPKERS
```

**Signal sequence.**

amino acids 1-20

**N-glycosylation sites.**

amino acids 120-124, 208-212

**Glycosaminoglycan attachment site.**

amino acids 80-84

**N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125